1/14

OIPE

RAW SEQUENCE LISTING DATE: 02/06/2002
PATENT APPLICATION: US/09/903,180A TIME: 09:21:55

Input Set : N:\Crf3\RULE60\09903180A.raw
Output Set: N:\CRF3\02062002\I903180A.raw


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 1 <110> APPLICANT: De Robertis, Edward M.
 2       Bouwmeester, Tewis
 3 <120> TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
 4       Factors
 5 <130> FILE REFERENCE: 510015-248
 6 <140> CURRENT APPLICATION NUMBER: US/09/903,180A
 7 <141> CURRENT FILING DATE: 2001-07-11
 8 <150> PRIOR APPLICATION NUMBER: 09/552,988
 9 <151> PRIOR FILING DATE: 2000-04-21
10 <150> PRIOR APPLICATION NUMBER: US 08/878,474
11 <151> PRIOR FILING DATE: 1997-06-18
12 <150> PRIOR APPLICATION NUMBER: US 60/020,150
13 <151> PRIOR FILING DATE: 1996-06-20
14 <160> NUMBER OF SEQ ID NOS: 10
15 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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18 <211> LENGTH: 270
19 <212> TYPE: PRT
20 <213> ORGANISM: Xenopus
21 <400> SEQUENCE: 1
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23         1               5                  10                  15
24        Asp Gly Ala Gly Lys His Ser Glu Gly Arg Glu Arg Thr Lys Thr Tyr
25                    20                  25                  30
26        Ser Leu Asn Ser Arg Gly Tyr Phe Arg Lys Glu Arg Gly Ala Arg Arg
27                35                  40                  45
28        Ser Lys Ile Leu Leu Val Asn Thr Lys Gly Leu Asp Glu Pro His Ile
29            50                  55                  60
30        Gly His Gly Asp Phe Gly Leu Val Ala Glu Leu Phe Asp Ser Thr Arg
31        65                  70                  75                  80
32        Thr His Thr Asn Arg Lys Glu Pro Asp Met Asn Lys Val Lys Leu Phe
33                        85                  90                  95
34        Ser Thr Val Ala His Gly Asn Lys Ser Ala Arg Arg Lys Ala Tyr Asn
35                    100                 105                 110
36        Gly Ser Arg Arg Asn Ile Phe Ser Arg Arg Ser Phe Asp Lys Arg Asn
37                115                 120                 125
38        Thr Glu Val Thr Glu Lys Pro Gly Ala Lys Met Phe Trp Asn Asn Phe
39            130                 135                 140
40        Leu Val Lys Met Asn Gly Ala Pro Gln Asn Thr Ser His Gly Ser Lys
41        145                 150                 155                 160
42        Ala Gln Glu Ile Met Lys Glu Ala Cys Lys Thr Leu Pro Phe Thr Gln
43                        165                 170                 175
44        Asn Ile Val His Glu Asn Cys Asp Arg Met Val Ile Gln Asn Asn Leu
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```
                  180                 185                 190
Cys Phe Gly Lys Cys Ile Ser Leu His Val Pro Asn Gln Gln Asp Arg
            195                 200                 205
Arg Asn Thr Cys Ser His Cys Leu Pro Ser Lys Phe Thr Leu Asn His
        210                 215                 220
Leu Thr Leu Asn Cys Thr Gly Ser Lys Asn Val Val Lys Val Val Met
225                 230                 235                 240
Met Val Glu Glu Cys Thr Cys Glu Ala His Lys Ser Asn Phe His Gln
                    245                 250                 255
Thr Ala Gln Phe Asn Met Asp Thr Ser Thr Thr Leu His His
                260                 265                 270
```

<210> SEQ ID NO: 2
<211> LENGTH: 1411
<212> TYPE: DNA
<213> ORGANISM: Xenopus
<400> SEQUENCE: 2

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gaattcctaa aagcggcaca gtgcaggaac agcaagtcgc tcagaaacac tgcagggtct      60
agatatcata caatgttact aaatgtactc aggatctgta ttatcgtctg ccttgtgaat     120
gatggagcag gaaaacactc agaaggacga gaaaggacaa aaacatattc acttaacagc     180
agaggttact tcagaaaaga aagaggagca cgtaggagca agattctgct ggtgaatact     240
aaaggtcttg atgaacccca cattgggcat ggtgattttg gcttagtagc tgaactattt     300
gattccacca gaacacatac aaacagaaaa gagccagaca tgaacaaagt caagcttttc     360
tcaacagttg cccatggaaa caaaagtgca agaagaaaag cttacaatgg ttctagaagg     420
aatatttttt ctcgccgttc ttttgataaa agaaatacag aggttactga aaagcctggt     480
gccaagatgt tctggaacaa ttttttggtt aaaatgaatg gagccccaca gaatacaagc     540
catggcagta aagcacagga aataatgaaa gaagcttgca aaaccttgcc cttcactcag     600
aatattgtac atgaaaactg tgacaggatg gtgatacaga acaatctgtg ctttggtaaa     660
tgcatctctc tccatgttcc aaatcagcaa gatcgacgaa atacttgttc ccattgcttg     720
ccgtccaaat ttaccctgaa ccacctgacg ctgaattgta ctggatctaa gaatgtagta     780
aaggttgtca tgatggtaga ggaatgcacg tgtgaagctc ataagagcaa cttccaccaa     840
actgcacagt ttaacatgga tacatctact accctgcacc attaaaagga ctgtctgcca     900
tacagtatgg aaatgcccat ttgttggaat attcgttaca tgctatgtat ctaaagcatt     960
atgttgcctt ctgtttcata taaccacatg gaataaggat tgtatgaatt ataattaaca    1020
aatggcattt tgtgtaacat gcaagatctc tgttccatca gttgcaagat aaaaggcaat    1080
atttgtttga ctttttttta caaaatgaat acccaaatat atgataagat aatggggtca    1140
aaactgttaa ggggtaatgt aataataggg actaacaacc aatcagcagg tatgatttac    1200
tggtcacctg tttaaaagca aacatcttat tggttgctat gggttactgc ttctgggcaa    1260
aatgtgtgcc tcatagggag gttagtgtgt tgtgtactga attaattgta tttatttcat    1320
tgttacaatg aagaggatgt ctatgtttat ttcacttttа ttaatgtaca ataaatgttc    1380
ttgtttcttt aaaaaaaaaa aaaaactcga g                                    1411
```

<210> SEQ ID NO: 3
<211> LENGTH: 318
<212> TYPE: PRT
<213> ORGANISM: Xenopus
<400> SEQUENCE: 3

```
Met Ser Arg Thr Arg Lys Val Asp Ser Leu Leu Leu Leu Ala Ile Pro
 1               5                  10                  15
Gly Leu Ala Leu Leu Leu Leu Pro Asn Ala Tyr Cys Ala Ser Cys Glu
            20                  25                  30
```

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```
Pro Val Arg Ile Pro Met Cys Lys Ser Met Pro Trp Asn Met Thr Lys
        35                  40                  45
Met Pro Asn His Leu His His Ser Thr Gln Ala Asn Ala Ile Leu Ala
    50                  55                  60
 Ile Glu Gln Phe Glu Gly Leu Leu Thr Thr Glu Cys Ser Gln Asp Leu
 65                  70                  75                  80
 Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys Thr Ile Asp Phe
                 85                  90                  95
 Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg
            100                 105                 110
 Ala Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His Thr Trp Pro Glu
        115                 120                 125
 Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile
    130                 135                 140
 Ser Pro Glu Ala Ile Val Thr Val Glu Gln Gly Thr Asp Ser Met Pro
 145                 150                 155                 160
 Asp Phe Ser Met Asp Ser Asn Asn Gly Asn Cys Gly Ser Gly Arg Glu
                 165                 170                 175
 His Cys Lys Cys Lys Pro Met Lys Ala Thr Gln Lys Thr Tyr Leu Lys
            180                 185                 190
 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Val
        195                 200                 205
 Lys Cys His Asp Ala Thr Ala Ile Val Glu Val Lys Glu Ile Leu Lys
    210                 215                 220
 Ser Ser Leu Val Asn Ile Pro Lys Asp Thr Val Thr Leu Tyr Thr Asn
 225                 230                 235                 240
 Ser Gly Cys Leu Cys Pro Gln Leu Val Ala Asn Glu Glu Tyr Ile Ile
                 245                 250                 255
 Met Gly Tyr Glu Asp Lys Glu Arg Thr Arg Leu Leu Leu Val Glu Gly
            260                 265                 270
 Ser Leu Ala Glu Lys Trp Arg Asp Arg Leu Ala Lys Lys Val Lys Arg
        275                 280                 285
 Trp Asp Gln Lys Leu Arg Arg Pro Arg Lys Ser Lys Asp Pro Val Ala
    290                 295                 300
 Pro Ile Pro Asn Lys Asn Ser Asn Ser Arg Gln Ala Arg Ser
 305                 310                 315

<210> SEQ ID NO: 4
<211> LENGTH: 1875
<212> TYPE: DNA
<213> ORGANISM: Xenopus
<400> SEQUENCE: 4
 gaattccctt tcacacagga ctcctggcag aggtgaatgg ttagccctat ggatttggtt      60
 tgttgatttt gacacatgat tgattgcttt cagataggat tgaaggactt ggatttttat     120
 ctaattctgc acttttaaat tatctgagta attgttcatt ttgtattgga tgggactaaa     180
 gataaactta actccttgct tttgacttgc ccataaacta taaggtgggg tgagttgtag     240
 ttgcttttac atgtgcccag attttccctg tattccctgt attccctcta aagtaagcct     300
 acacatacag gttgggcaga ataacaatgt ctcgaacaag gaaagtggac tcattactgc     360
 tactggccat acctggactg gcgcttctct tattacccaa tgcttactgt gcttcgtgtg     420
 agcctgtgcg gatccccatg tgcaaatcta tgccatggaa catgaccaag atgcccaacc     480
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```
146        atctccacca cagcactcaa gccaatgcca tcctggcaat tgaacagttt gaaggtttgc     540
147        tgaccactga atgtagccag gacctttttgt tctttctgtg tgccatgtat gccccccattt    600
148        gtaccatcga tttccagcat gaaccaatta agccttgcaa gtccgtgtgc gaaagggcca      660
149        gggccggctg tgagcccatt ctcataaagt accggcacac ttggccagag agcctggcat      720
150        gtgaagagct gcccgtatat gacagaggag tctgcatctc cccagaggct atcgtcacag      780
151        tggaacaagg aacagattca atgccagact tctccatgga ttcaaacaat ggaaattgcg      840
152        gaagcggcag ggagcactgt aaatgcaagc ccatgaaggc aaccccaaaag acgtatctca     900
153        agaataatta caattatgta atcagagcaa aagtgaaaga ggtgaaagtg aaatgccacg      960
154        acgcaacagc aattgtggaa gtaaaggaga ttctcaagtc ttcctagtg aacattccta      1020
155        aagacacagt gacactgtac accaactcag gctgcttgtg ccccagctt gttgccaatg      1080
156        aggaatacat aattatgggc tatgaagaca aagagcgtac caggcttcta ctagtggaag     1140
157        gatccttggc cgaaaaatgg agagatcgtc ttgctaagaa agtcaagcgc tgggatcaaa      1200
158        agcttcgacg tcccaggaaa agcaaagacc ccgtggctcc aattcccaac aaaaacagca      1260
159        attccagaca agcgcgtagt tagactaacg gaaaggtgta tggaaactct atggactttg      1320
160        aaactaagat ttgcattgtt ggaagagcaa aaaagaaatt gcactacagc acgttatatt      1380
161        ctattgttta ctacaagaag ctggtttagt tgattgtagt tctcctttcc ttctttttt      1440
162        ttataactat atttgcacgt gttcccaggc aattgtttta ttcaacttcc agtgacagag      1500
163        cagtgactga atgtctcagc ctaaagaagc tcaattcatt tctgatcaac taatggtgac      1560
164        aagtgtttga tacttgggga aagtgaacta attgcaatgg taaatcagag aaaagttgac      1620
165        caatgttgct tttcctgtag atgaacaagt gagagatcac atttaaatga tgatcacttt      1680
166        ccatttaata ctttcagcag ttttagttag atgacatgta ggatgcacct aaatctaaat      1740
167        attttatcat aaatgaagag ctggtttaga ctgtatggtc actgttggga aggtaaatgc      1800
168        ctactttgtc aattctgttt taaaaattgc ctaaataaat attaagtcct aaataaaaaa      1860
169        aaaaaaaaaa aaaaa                                                       1875
171 <210> SEQ ID NO: 5
172 <211> LENGTH: 979
173 <212> TYPE: PRT
174 <213> ORGANISM: Xenopus
175 <400> SEQUENCE: 5
176        Met Leu Leu Leu Phe Arg Ala Ile Pro Met Leu Leu Leu Gly Leu Met
177         1               5                  10                  15
178        Val Leu Gln Thr Asp Cys Glu Ile Ala Gln Tyr Tyr Ile Asp Glu Glu
179                    20                  25                  30
180        Glu Pro Pro Gly Thr Val Ile Ala Val Leu Ser Gln His Ser Ile Phe
181                35                  40                  45
182        Asn Thr Thr Asp Ile Pro Ala Thr Asn Phe Arg Leu Met Lys Gln Phe
183            50                  55                  60
184        Asn Asn Ser Leu Ile Gly Val Arg Glu Ser Asp Gly Gln Leu Ser Ile
185        65                  70                  75                  80
186        Met Glu Arg Ile Asp Arg Glu Gln Ile Cys Arg Gln Ser Leu His Cys
187                        85                  90                  95
188        Asn Leu Ala Leu Asp Val Val Ser Phe Ser Lys Gly His Phe Lys Leu
189                    100                 105                 110
190        Leu Asn Val Lys Val Glu Val Arg Asp Ile Asn Asp His Ser Pro His
191                115                 120                 125
192        Phe Pro Ser Glu Ile Met His Val Glu Val Ser Glu Ser Ser Ser Val
193            130                 135                 140
194        Gly Thr Arg Ile Pro Leu Glu Ile Ala Ile Asp Glu Asp Val Gly Ser
195        145                 150                 155                 160
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```
196  Asn Ser Ile Gln Asn Phe Gln Ile Ser Asn Asn Ser His Phe Ser Ile
197                  165                 170                 175
198  Asp Val Leu Thr Arg Ala Asp Gly Val Lys Tyr Ala Asp Leu Val Leu
199              180                 185                 190
200  Met Arg Glu Leu Asp Arg Glu Ile Gln Pro Thr Tyr Ile Met Glu Leu
201          195                 200                 205
202  Leu Ala Met Asp Gly Gly Val Pro Ser Leu Ser Gly Thr Ala Val Val
203      210                 215                 220
204  Asn Ile Arg Val Leu Asp Phe Asn Asp Asn Ser Pro Val Phe Glu Arg
205  225                 230                 235                 240
206  Ser Thr Ile Ala Val Asp Leu Val Glu Asp Ala Pro Leu Gly Tyr Leu
207                  245                 250                 255
208  Leu Leu Glu Leu His Ala Thr Asp Asp Asp Glu Gly Val Asn Gly Glu
209              260                 265                 270
210  Ile Val Tyr Gly Phe Ser Thr Leu Ala Ser Gln Glu Val Arg Gln Leu
211          275                 280                 285
212  Phe Lys Ile Asn Ser Arg Thr Gly Ser Val Thr Leu Glu Gly Gln Val
213      290                 295                 300
214  Asp Phe Glu Thr Lys Gln Thr Tyr Glu Phe Glu Val Gln Ala Gln Asp
215  305                 310                 315                 320
216  Leu Gly Pro Asn Pro Leu Thr Ala Thr Cys Lys Val Thr Val His Ile
217                  325                 330                 335
218  Leu Asp Val Asn Asp Asn Thr Pro Ala Ile Thr Ile Thr Pro Leu Thr
219              340                 345                 350
220  Thr Val Asn Ala Gly Val Ala Tyr Ile Pro Glu Thr Ala Thr Lys Glu
221          355                 360                 365
222  Asn Phe Ile Ala Leu Ile Ser Thr Thr Asp Arg Ala Ser Gly Ser Asn
223      370                 375                 380
224  Gly Gln Val Arg Cys Thr Leu Tyr Gly His Glu His Phe Lys Leu Gln
225  385                 390                 395                 400
226  Gln Ala Tyr Glu Asp Ser Tyr Met Ile Val Thr Thr Ser Thr Leu Asp
227                  405                 410                 415
228  Arg Glu Asn Ile Ala Ala Tyr Ser Leu Thr Val Val Ala Glu Asp Leu
229              420                 425                 430
230  Gly Phe Pro Ser Leu Lys Thr Lys Lys Tyr Tyr Thr Val Lys Val Ser
231          435                 440                 445
232  Asp Glu Asn Asp Asn Ala Pro Val Phe Ser Lys Pro Gln Tyr Glu Ala
233      450                 455                 460
234  Ser Ile Leu Glu Asn Asn Ala Pro Gly Ser Tyr Ile Thr Thr Val Ile
235  465                 470                 475                 480
236  Ala Arg Asp Ser Asp Ser Asp Gln Asn Gly Lys Val Asn Tyr Arg Leu
237                  485                 490                 495
238  Val Asp Ala Lys Val Met Gly Gln Ser Leu Thr Thr Phe Val Ser Leu
239              500                 505                 510
240  Asp Ala Asp Ser Gly Val Leu Arg Ala Val Arg Ser Leu Asp Tyr Glu
241          515                 520                 525
242  Lys Leu Lys Gln Leu Asp Phe Glu Ile Glu Ala Ala Asp Asn Gly Ile
243      530                 535                 540
244  Pro Gln Leu Ser Thr Arg Val Gln Leu Asn Leu Arg Ile Val Asp Gln
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VERIFICATION SUMMARY DATE: 02/06/2002
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Input Set : N:\Crf3\RULE60\09903180A.raw
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